

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 15:51:16 : Search time 172.18 Seconds
(without alignments)
471.220 Million cell updates/sec

Title: US-09-052-089a-1
Perfect score: 2384
Sequence: 1 MPRLCTICSDPFDHSDRV.....VRKTVPSLQAKLDTFLWS 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	2384	100.0	469	4	000467
2	2357	98.9	469	4	Q9BW62
3	1870.5	78.5	470	11	Q9C6P4
4	1847.5	77.5	470	11	Q08854
5	955	40.1	223	13	Q922M8
6	925	38.8	433	13	Q9YGN2
7	291.5	12.2	435	5	Q95S55
8	286.5	12.0	435	5	Q9V8D7
9	204.5	8.6	506	10	Q9M143
10	188	7.9	1530	4	Q43241
11	185.5	7.8	1930	13	Q9DGD5
12	182	7.6	425	5	P90990
13	182	7.6	1578	10	Q9AY25
14	181	7.6	1931	13	Q42352
15	181	7.6	1958	5	Q96062
16	180	7.6	1092	13	Q90338

17	179	7.5	477	4	Q9Y577
18	179	7.5	1138	5	Q22276
19	178.5	7.5	764	13	Q91411
20	178	7.5	477	11	Q9WV59
21	177.5	7.4	948	4	Q9UK7
22	177.5	7.4	1133	5	Q21022
23	177.5	7.4	1305	10	Q9FJ35
24	177.5	7.4	1933	13	Q90337
25	177	7.4	879	13	Q9YHD8
26	176.5	7.4	976	11	Q9SM12
27	176.5	7.4	1156	17	Q28714
28	176	7.4	1156	16	Q66878
29	176	7.4	1939	6	Q9TV61
30	175.5	7.4	1429	13	Q98T05
31	175.5	7.4	2473	11	Q9Q284
32	175	7.3	1690	5	Q44929
33	174.5	7.3	529	4	Q9UP51
34	174.5	7.3	1119	13	P87344
35	174	7.3	671	13	Q9YHD4
36	173.5	7.3	975	13	Q98T05
37	173.5	7.3	1743	5	Q96063
38	173	7.3	437	2	Q9AMC4
39	173	7.3	1120	11	Q99M11
40	172.5	7.2	708	13	Q9YHD7
41	172.5	7.2	1936	13	Q90YF6
42	172.5	7.2	1938	13	Q91BD7
43	171.5	7.2	592	2	Q914N1
44	171.5	7.2	1938	6	Q9G3P9
45	171.5	7.2	1999	11	Q63731

ALIGNMENTS

RESULT	ID	000467	PRELIMINARY;	PRT;	469 AA.
AC	000467;				
DT	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	HTIRIP.				
GN	HTIRIP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97258620; PubMed=9104814;				
RA	Lee S.Y., Lee S.Y., Choi Y.,				
RT	"TRAF-Interacting protein (TRIP): a novel component of the tumor				
RT	necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes				
RT	that inhibits TRAF2-mediated NF-kappa activation."				
RL	J. Exp. Med. 185:1275-1285(1997).				
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				
DR	EMBL, U77845; AAB52993.1; -				
DR	InterPro: IPR001841; Znf_Fing.				
DR	Pfam: PF00097; zf-C3HC4; 1.				
DR	SMART: SM00184; RING; 1.				
KW	Zinc-finger.				
SQ	SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABAE4 CRC64;				

Query Match 100.0%; Score 2384; DB 4; Length 469;
Best local similarity 100.0%; Pred. No. 1.7e-121;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRLCTICSDPFDHSDVAHICGHTFHLOCIOSFEFAPSTCCRCRQVCKRTIIN 60
DB 1 MPRLCTICSDPFDHSDVAHICGHTFHLOCIOSFEFAPSTCCRCRQVCKRTIIN 60
QY 61 KLFPDLAEEENVDREFLKNELNDVRAQLSQDKERKRDQSVIIDTJLRDTLEERNATVVS 120

Db 61 KLFDLAEEENVDREFLNKNELDVNRRAQLSQDKKEKDSQVITDTRDTLEERNATVVS 120
Qy 121 LQOALGKAEMLCSTLKQKMKYLEQOODETKOAEAGRLSRMKMTEOIELLOSOLEPVE 180
Db 121 LQOALGKAEMLCSTLKQKMKYLEQOODETKOAEAGRLSRMKMTEOIELLOSOLEPVE 180
Qy 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Db 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Qy 241 SELDOAKLELSAOKDLOSADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Db 241 SELDOAKLELSAOKDLOSADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Qy 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSOHGYEKLCEKSHSPIDVPKICKGP 360
Db 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSOHGYEKLCEKSHSPIDVPKICKGP 360
Qy 361 RRESQSLSGGSCAGEPDEELVGAFPIFVRNAILGQOKPKRPRSSESSKDVVTRTGFGL 420
Db 361 RRESQSLSGGSCAGEPDEELVGAFPIFVRNAILGQOKPKRPRSSESSKDVVTRTGFGL 420
Qy 421 GGRKFTIOPTDTVMIRPLPVKPKTKVQORVVKTVPSLFOAKLDTFLMS 469
Db 421 GGRKFTIOPTDTVMIRPLPVKPKTKVQORVVKTVPSLFOAKLDTFLMS 469

RESULT 2
Q9BMF2 ID Q9BMF2 PRELIMINARY; PRT; 469 AA.
AC Q9BMF2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LONG CARCINOMA;
RA Strausberg R.;
RL Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: BC000310; AAH00310.1; -
DR InterPro: IPR001841; Znf_Ting.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Znnc-finger.
SQ SEQUENCE 469 AA: 53294 MW: B9EF3808FBC5985B CRC64;

Query Match 98.9%; Score 2357; DB 4; Length 469;
Best Local Similarity 99.1%; Pred. No. 4.8e-120;
Matches 465; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPRALCTICSDFFDHSRDVAIHGHTFHLCQLIOSETAPSRCTQCRCRIQVQKRTIIN 60
Db 1 MPRALCTICSDFFDHSRDVAIHGHTFHLCQLIOSETAPSRCTQCRCRIQVQKRTIIN 60
Qy 61 KLFDLAEEENVDREFLNKNELDVNRRAQLSQDKKEKDSQVITDTRDTLEERNATVVS 120
Db 61 KLFDLAEEENVDREFLNKNELDVNRRAQLSQDKKEKDSQVITDTRDTLEERNATVVS 120
Qy 121 LQOALGKAEMLCSTLKQKMKYLEQOODETKOAEAGRLSRMKMTEOIELLOSOLEPVE 180
Db 121 LQOALGKAEMLCSTLKQKMKYLEQOODETKOAEAGRLSRMKMTEOIELLOSOLEPVE 180
Qy 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240
Db 181 EEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRLKDLFSSRSKLQTVY 240

Qy 241 SELDOAKLELSAOKDLOSADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Db 241 SELDOAKLELSAOKDLOSADKEIMSLKKLTMLQETLNPVASETVDRLVLESAPAVE 300
Qy 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSOHGYEKLCEKSHSPIDVPKICKGP 360
Db 301 VNLKLRPSFRDDIDLNTFPDVPAPPASSOHGYEKLCEKSHSPIDVPKICKGP 360
Qy 361 RRESQSLSGGSCAGEPDEELVGAFPIFVRNAILGQOKPKRPRSSESSKDVVTRTGFGL 420
Db 361 RRESQSLSGGSCAGEPDEELVGAFPIFVRNAILGQOKPKRPRSSESSKDVVTRTGFGL 420
Qy 421 GGRKFTIOPTDTVMIRPLPVKPKTKVQORVVKTVPSLFOAKLDTFLMS 469
Db 421 GGRKFTIOPTDTVMIRPLPVKPKTKVQORVVKTVPSLFOAKLDTFLMS 469

RESULT 3
Q9CP4 ID Q9CP4 PRELIMINARY; PRT; 470 AA.
AC Q9CP4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kusunawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaka S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AK012948; BAB28567.1; -
DR MGD: MGI:1096377; Traip.
DR InterPro: IPR001841; Znf_Ting.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Znnc-finger.
SQ SEQUENCE 470 AA: 53149 MW: EBFAC49A9F4BP2E CRC64;

Query Match 78.5%; Score 1870.5; DB 11; Length 470;
Best Local Similarity 79.1%; Pred. No. 9.2e-94;
Matches 370; Conservative 42; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MPRALCTICSDFFDHSRDVAIHGHTFHLCQLIOSETAPSRCTQCRCRIQVQKRTIIN 60
Db 1 MPRALCTICSDFFDHSRDVAIHGHTFHLCQLIOSETAPSRCTQCRCRIQVQKRTIIN 60

DE TRAF INTERACTING PROTEIN.
 GN TRIP.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99148833; PubMed=10025966;
 RA Coltage A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M.,
 RA Elgar G.,
 RT "Three receptor genes for plasmalogen related growth factors in the
 RT genome of the puffer fish Fugu rubripes."
 RL FBS Lett. 443:370-374(1999).
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AJ010317; CA09084.1; -
 DR InterPro: IPR001841; Znf_1ing.
 DR Pfam: PF00097; zf-C3HC4.1.
 DR SMART: SM00184; RING; 1.
 DR Zinc-finger
 KW
 SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match 38.8%; Score 925; DB 13; Length 433;
 Best Local Similarity 43.8%; Pred. No. 9.8e-43;
 Matches 197; Conservative 76; Mismatches 121; Indels 56; Gaps 5;

QY 1 MPRLCTGSDFFDHSRDVAIHGHTFHLOCLIOSEFTAPSRTPCPCRIQVSKRTIIN 60
 DB 1 MPRLAQTGSDFFDHSRDVAIHGHTFHHECLVRFMGQTAPKTCPCRCQVSTRHIS 60
 QY 61 KLFEDLAQEEENVLDREFLKNELDNVRAQLSKDKERKDSQVITDRLDTEENATVVS 120
 DB 61 KLFYDGLDSSVGDPELQNELDRVKNVFSKERDMEKQKAMDLMETVELQKALEN 120
 QY 121 LQALGRAEMLCSTLKQKMYLEQODETKQAOEAGRLSRKMKMTWEOIELLOSOLEPV 180
 DB 121 LQKVMKEKCKSALRQMTYLEQSHNDTRAKAEVRLRKMTPESLDVYLOGQRAEV 180
 QY 181 EEMIRDMGVGSAVEQLAVYCVSLKKEVENLEKARKASGEVADLRDLFSSRSKLOTYV 240
 DB 181 ESMITDMGIGQAAVEQLSICISLKEEDNKLGLKSSNEMCEKLRKEVLSNNKLKAL 240
 QY 241 SELDQALTELKSAQKQDLSADKELMSLKKLTWLOETLNPVASEVYVDRLVE--SPAP 298
 DB 241 LELTKADDMKSLQNDLNLNKEKISLKKVEFLQELALSTPTRTNEALGRLLFERCGAP 300
 QY 299 -----VEVNLKLRSPFRDDIDLNATFDVDTPPARPSSSQHGVEKLCLEKSHSPIDVP 353
 DB 301 PONSRYVSKAGCLHPSPSNGEDIDLNMTYDTPP-----DDVR 336
 QY 354 KKTICKGPRKESQSLSGQSCAGEPEDELVGAFPIEVNAILGOKOPRPNSESSCSKDVV 413
 DB 337 KRPKQVSKKMKHL-----DSVILLTRTKYKNLVSNQK-----FV 371
 QY 414 RTGFDGLGGRKFTQPTDWTMIRPLPYKPK 443
 DB 372 QSGYDGLGGRKFTQPTTHAVRSEASKPE 401

RESULT 7
 095SSS PRELIMINARY; PRT; 435 AA.
 AC 095SSS;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GH03577P.
 GN CG5140.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wen K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060610; AAL28158.1; -
 SQ SEQUENCE 435 AA; 48455 MW; 0BFFOAGC1DD9416E CRC64;

Query Match 12.2%; Score 291.5; DB 5; Length 435;
 Best Local Similarity 25.1%; Pred. No. 1.6e-08;
 Matches 113; Conservative 82; Mismatches 161; Indels 95; Gaps 18;

QY 7 CTGSDFFDHSRDVAIHGHTFHLOCLIOSEFTAPSRTPCPCRIQVSKRTIINKLEFDL 66
 DB 6 CVICAELEFGQADEVFATVCGMFHNLCLNDQLDR--SKTCPCQCKNKTTRNIF-RVYFNL 62
 QY 67 AQEENVLDREFLKNELDNVRAQLSKDKERKDSQVITDRLDTEENATVVSILQALG 126
 DB 63 ANDVSHIDVGSLOEOLDNMLSMKMYEKERNDEQIIRDLKETQKCLTIAGLEKQV 122
 QY 127 KAEMLCSTLKQKMYLEQODETKQAOEAGRLSRKMKMTWEOIELLOSOLEPEVEMIRD 186
 DB 123 KQDELISVYEQIGVLKSDAHVVDGLRKENKTKLSQISMEGISAIIAASADADRLKN 182
 QY 187 MGVGSAVEQLAVYCVSLKKEVENLEKARKASGEVADLRDLFSSRSKLOTYSE 242
 DB 183 -----EADPHVLANVSTLKLROCESKTKTELNVKVVONDLKTEELAR-KLEERVSH 237
 QY 243 LD-----QAKL--ELKSAQKQDLSA-----DKEIMSLKRLTWLOETLNPVASETV 289
 DB 238 LESDLYAQEKIQAFKFTAVLDSPNASCGLNSIILALKE--EKRITISPTVKNIK 293
 QY 290 RLVESPAVYEVNLKLRSPFRDDIDLNATFDVDTPPARPSSSQHGVE-----KICLE 343
 DB 294 R-IEESTSPY-LNIK-----SSSVGLAHLNLTGNIGLA 325
 QY 344 KSH-SPIQDVPKIKCKPRKESQSLSGQSCAG-----EPDEELVGAPPIVNAAILGOK 398
 DB 326 KSKISPIKGV-----GVSKTSTIRTKTSSDISEKISIF-----K 362
 QY 399 PKRPRSESSCSKDVVRG---FDGLGGRK 425
 DB 363 PRLLIGSSSSALATATGSNPNVYMGMSSEK 393

RESULT 8
 09VBD7 PRELIMINARY; PRT; 455 AA.
 AC 09VBD7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CG5140 PROTEIN.
 GN CG5140.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,


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AC 042352;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
NC NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RX MEDLINE=97352533; Pubmed=9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle."
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 1931 AA; 221162 MW; 59466B7BD0872DDD CRC64;

Query Match 7.6%; Score 181; DB 13; Length 1931;
Best Local Similarity 21.2%; Pred. No. 0.075;
Matches 92; Conservative 80; Mismatches 163; Indels 98; Gaps 16;

QY 31 LQCLISFETAPSRCTQCRCRIQVGGKRTIINKLPFDLAQEEBNVLDREF----- 78
DB 1141 LEEISERLERLEGAGTAAQIEMNKKREADFQKMRDL---EESTLQHEATAAALRKKQADT 1197
QY 79 ---LKNLDNVNRAQLSQDKCKRDSOVIITDLRPTLEERNATVYSLQALGKAMGLSTL 135
DB 1198 VAELEGEDIDNIQRYKKQKLEKESEYKMEIDDLISNME-----AVAKAGNLEKMCRTL 1250
QY 136 KQMKYLYEQOQDETQAQOEAGRLRSKMT-----MEQIELLOSQLP----- 178
DB 1251 EDOLSEIKAKSDENSRQLNMNQRARLQTENGEFSRQLBEKALV-SQLTRGQAFITQ 1309
QY 179 -----EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASEVADKLKDLFSS 232
DB 1310 IEDLQRHVEEVEVAKNALAAVQSAHDCDLLEQYEEQEAETELORGSKANSEVAQW 1369
QY 233 RSKLQI---VSELDQAQKLELSAQDKLOSARKETMSLKKKLTLMQETLNLPPVASETV 288
DB 1370 RAYETDAIQRTEBLEAKKRL-AQR-LQDAEESIEAVSSKASCTEKTQ--RLQGEVE 1424
QY 289 DRLV-LESPAPVENLKLRRPSFRDDI-----DLNLTFFDVDPAPPSSQ----- 333
DB 1425 DLWIDGRANAALANLDKQRNF-DKVLAEWKQKYESSQADELEAKQEAASISLELFPKM 1483
QY 334 HGYYEKI---CLEKSHSPIQ-----DVPKTKCKPPRESQSLIG 369
DB 1484 NSYEALDHLFETLKREKNKLQOEISDLSQELGTGKSHLEKAKKIVSEKAEIQTALE 1543
QY 370 GQSCAGEPDEELV 382
DB 1544 EAESTLEHESKI 1556
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RESULT 15
ID 096062 PRELIMINARY; PRT: 1958 AA.
AC 096062;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
CN D1MHC-A.
OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Dugesia.
NC NCBI_TaxID=6161;
RN [1]
RP SEQUENCE FROM N.A.
RA Kobayashi C., Kobayashi S., Oril H., Agata K., Watanabe K.;
RT "Identification of two distinct myosins in the planarian, Dugesia
RT japonica, by the expression of myosin heavy chain genes."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB015484; BAA34954.1; -.
DR HSSP: P24733; 1WDC.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR001637; Glna_adenylin.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00182; GlnA_ADENYLATION; UNKNOWN_1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1958 AA; 224857 MW; 3FE254327DF89524 CRC64;

Query Match 7.6%; Score 181; DB 5; Length 1958;
Best Local Similarity 21.9%; Pred. No. 0.077;
Matches 66; Conservative 66; Mismatches 106; Indels 64; Gaps 9;

QY 60 NKLFDLAQEEBNVLDREFLKNELDNVRAQLSQDKCKRDS-----QVIIDTLR 108
DB 878 NDFLQIQTEQDSLDAAEEKVSKLVNQKADMESRIKELEDHLLBEEDASAGLEMKKMQ 937
QY 109 DTLEERNATVYSLQALGKAMGLSTLKKQMKYLYEQOQDETQAQOEAGRLRSKMTMEQ 168
DB 938 GEIEELKQDVDESSLOKAEOKETAKDOQIKAL---QDQIAQEEEMNKKKEKKADE 994
QY 169 IELLQSOLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASEVADKLKRD 228
DB 995 LQKTEESLOAEEEKVANKLAKAKLEQ-----TIDEMEENLSREQKVADV-EKYKK 1047
QY 229 LFSRSKLIQTIVYSELDAKLE---LKSQDKLQSA-----DKETMSLKKK 270
DB 1048 IETELKQTEQTVDDLEVKRKELEQQLKRMELSNMSSKTEDSGVLAQQLKKIKELQAR 1107
QY 271 LTMQETL-----NLPPVASETVDRVLE---SPAPYEVN-----LKL 305
DB 1108 IOELEEDLEAEORAKAERKSRQLGEGELELSDRLEEQGATSAOLELKKKREAEELKL 1167
QY 306 RR 307
DB 1168 KR 1169

RESULT 16
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Q90338
ID Q90338 PRELIMINARY; PRT; 1092 AA.
AC Q90338;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOIN HEAVY CHAIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_Taxid=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RX MEDLINE=9716447; PubMed=9023993;
RA Imai J., Hirayama Y., Kikuchi K., Kakimura M., Watabe S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
muscle and their gene expression associated with temperature
acclimation.";
RT J. Exp. Biol. 200:27-34(1997).
RL EMBL: D50475; BAA09068.1; -;
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR NON TER 1
SQ SEQUENCE 1092 AA; 125885 MW; B6BABA3963BEBA CRC64;

Query Match 7.6%; Score 180; DB 13; Length 1092;
Best Local Similarity 23.5%; Pred. No. 0.046;
Matches 68; Conservative 57; Mismatches 108; Indels 56; Gaps 9;

QY 31 LQCLISFETAPSTCQCRCRQVCKRTIINKLFPDLAEOEENVLDREF----- 78
DB 302 LEEISELEEREGATAOIEKMKREADFOKMRDL--EESTQHETATAALRKQADT 358
QY 79 ---LKNELDNVRAQLSOKDEKRDQSVIIDLRLDTEERNATVVSLOALGKAMLCSTL 135
DB 359 VAEIGEDIDNLQRYKQKLEKSEYKMEIDLTSMNE-----AVAKAGNLEKMCRTL 411
QY 136 KKOAKYLEQOODETKAOAEAGRLSKMKT-----MEQIELLSQLP----- 178
DB 412 EDQLSEIKAKSDENSRLNDWNAQRARLQTFNGEFSSRLKEKALV--SQLRGQAFTQ 470
QY 179 -----EVEEKIRDMGVGSQSAVEQLAVYCVSLKKEYLEKARKASGEVADKLKDLFSS 232
DB 471 IEDLQRRHVEEVRKKNALAHAVOSARHDCDLRLQYEEDQAKTELOGMSKANSEVAOW 530
QY 233 RSKLQIQT---VYSELDOAKLELKSQKDLQSGADKEIMSLKKLMLQET 277
DB 531 RAKETDAIQRTLELEFAKKKL--AQR-LQDAEESIEAVSSKASLEKT 576

RESULT 17
Q9Y577
ID Q9Y577 PRELIMINARY; PRT; 477 AA.
AC Q9Y577;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RING FINGER PROTEIN TERF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=99011410; PubMed=9792805;
RA Ogawa S., Goto W., Oritomo A., Hosoi T., Ouchi Y., Muramatsu M.,
Inoue S.;

RT "Molecular cloning of a novel RING finger-B box-coiled coil (RBCC)
RT protein, terf, expressed in the testis.";
RL Biochem. Biophys. Res. Commun. 251:515-519(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ogawa S., Goto W., Oritomo A., Hosoi T., Ouchi Y., Muramatsu M.,
Inoue S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF156271; AAD40286.1; -;
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
DR InterPro: IPR000315; Znf_box.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; Zf-B_box; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR ZINC_FINGER.
SQ SEQUENCE 477 AA; 54418 MW; ECA4010661ADD28A CRC64;

Query Match 7.5%; Score 179; DB 4; Length 477;
Best Local Similarity 25.3%; Pred. No. 0.021;
Matches 84; Conservative 56; Mismatches 132; Indels 60; Gaps 14;

QY 5 ALCTICGDFPHSDVAIHGHTFHLOCLQSFETAPSR-----TQPCRCRYGV 54
DB 14 ATCSICLDYF---TDVWTTGTHNFCRACIQLSWEKARGKRRKRGSPPCPCRENSP 70
QY 55 KRITII-NKLFEDLAQ--EENVDLREFLNELDNVRAQLSOKDEKRDQSVIIDLRLDTL 111
DB 71 QRNLPLRNLTKVAMQOHGLOKODLQCEHNEPLKFCQKDDSP-----ICVVCESR 125
QY 112 EERNATVVSLOALGKAMLCSTLKKOKYLEQODET--KQAOEAGRLSKMKTMEQI 169
DB 126 EHRHLRVLPAAEAVQGYKL--KLEEDMEYLRQITRTGNLQAREEOSLAWECKVERR 182
QY 170 ELLLOSLPEVEEIRDMGVGSQSAVEQLAVYCVSLKKEYLEKARKASGEVADKLKDL 229
DB 183 ERIVLE-----FEKKNLYLV--EEQRLQLALETBEETASRLRNSV 222
QY 230 FSSRSKLQTVYSELDOAKLELKSQKDLQSGAD--KEIMSLKKLMLQETLNLPPVASET 287
DB 223 ACLDRQGHSL--ELLLLQLERSYQGPLQMDKKEPLSRKNV-----SVQCEVAPPT 275
QY 288 VDRLVLESPAVEYNLKRPSFRDIDLNT 319
DB 276 RPRTVCRVPGQIEV--LR-GFLEDVVPDAT 302

RESULT 18
Q22276
ID Q22276 PRELIMINARY; PRT; 1138 AA.
AC Q22276; Q22276;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE TORC4.10 PROTEIN.
GN TORC4.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Buck D., Berks M.;

DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
 KW ZINC-finger
 SQ SEQUENCE 477 AA; 54954 MW; 1AAB42BB02615ADF CRC64;

Query Match 7.5%; Score 178; DB 11; Length 477;
 Best Local Similarity 25.8%; Pred. No. 0.024;
 Matches 86; Conservative 61; Mismatches 114; Indels 72; Gaps 18;

QY 5 ALCTICDFDHSRDVAIHGHTFHLQCLIQSFETAPSR-----TCPCRIQVG 54
 DB 14 ATCSICLDYF---TDPMWACGHNFCECQIOMSEKKGKGGKKKGKSGPCEGEMSP 70
 QY 55 KRPI-INKLF---FDLAQEEENVLDREFLNELDNVPAQISQDKF---KRSQVITDTL 107
 DB 71 QRNLPRRLTLTKVAEMARHPGLHKRDL-----CQIHQEFLLKFCDDQDPICVVC 121
 QY 108 RDTLEERNATVVSLOALGKAEMLCSTLKQMKYLT--EQODETKOAEAGRLRSKMT 165
 DB 122 REAOEHMHRVLPDEAREKLT---RLEEDIKLREEMKTTETLQAKKEOTLTMOERV 178
 QY 166 MEQIELLQSQLPVEEEMIRDMVGOSAVQLAVYCVSLKKEYENLKEARKAGEVADKL 225
 DB 179 KERERILE---EFQKVLFLEF-----VEBERRLQILKKEED-----DTL 215
 QY 226 RKDLFSSRSKIQTYSELDQAKLEL--KSAOKDQASD--KEINSLKKTLMLOETLNP 281
 DB 216 GK-LQDSKASLDHQSRSLDILLQLEBOTEOPLQMDVKTDLTKRESLSMOYPEVVL- 273
 QY 282 PVASETVRLVLESPAPVEVNLKLRPSFRDI 314
 DB 274 PVAIKYCRV---PGQIEV-LK-----SFQEDV 297

RESULT 21
 ID 09UIK7 PRELIMINARY; PRT; 948 AA.
 AC 09UIK7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ELKS.
 GN ELKS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakata T.
 RT "Fusion of a Novel Gene, ELKS, to c-ret in a Papillary Thyroid Carcinoma."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015617; BAA8763.1; -
 DR InterPro: IPR002017; Spectrin.
 SQ SEQUENCE 948 AA; 108792 MW; 34A297FDFC9F7602 CRC64;

Query Match 7.4%; Score 177.5; DB 4; Length 948;
 Best Local Similarity 20.3%; Pred. No. 0.054;
 Matches 83; Conservative 80; Mismatches 135; Indels 111; Gaps 14;

QY 8 TICSDFFDHSRDVAIHGHTFHLQCLIQSFETAPSRTPCQRIQVG-----KRTII 59
 DB 463 TLTRQFSDSKO-----HIEVLKESL-TAKEQRAALIQTEVVALRLLEKETML 510
 QY 60 N---KLEFDLAQEE-----ENVLDRE-----FLKNDLVNRAQLSQDKERKRSQ 101
 DB 511 NKTKKQIQDNMAEKGTOAGELHDKMDVAKERKVNVLQKTIENLQEQLRDKERQMSLK 570
 QY 102 VIIDLRLTEERNATVVSLOALGKAEMLCSTLKQMKYLEOQODETKOAEAGRLRS 161

DB 571 ERVKSLOADTNTNIDTALTTLEALAEKERIERLTK-----EQRDEREKGQEIINYKK 624
 QY 162 KMTMEQIELLQSQLPVEEEMIRDMVGOS-----AVEQLAVCV- 202
 DB 625 DLKDLKEKVSLLQDSEKASLIDLKEHASSLASSGLKRSRLKLTLEIQKKEECLK 684
 QY 203 ---SIKKEYENLKEARKAGEVADK---LRKDLFSSRSKIQTYSELDQAKLELKSQKD 256
 DB 685 MESQLKAHEALAEAR-ASPMSDRIOHLERITRKDESSKAQAEVLDLLETLEKEYNE 743
 QY 257 LQSNADKEIMSL-----KKKLTMLQETLNPVASETVDR 290
 DB 744 KNDKDKIALELSITSNQVQDKKKVANLKHKGQVEKKKSAQMLKEARRREDNLNDSQ 803
 QY 291 LVLESPAPVEVNLKLRPSFRDIDLNATFDVTPPARPSSQHGYYEK 339
 DB 804 LOVE-----ELLMAMEK-----VKQELSEMKAKLSSTOOSLAEK 837

RESULT 22
 ID 021022 PRELIMINARY; PRT; 1133 AA.
 AC 021022; Q21071;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE F59A2.6 PROTEIN.
 GN F59A2.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lightning J.
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z34801; CAA84332.1; -
 DR EMBL; Z66514; CAA84332.1; JOINED.
 DR EMBL; Z66514; CAA91344.1; -
 DR EMBL; Z34801; CAA91344.1; JOINED.
 DR InterPro: IPR000237; GRIP.
 DR Pfam: PF01465; GRIP; 1.
 SQ SEQUENCE 1133 AA; 129239 MW; 92015E790A9DE01F CRC64;

Query Match 7.4%; Score 177.5; DB 5; Length 1133;
 Best Local Similarity 20.5%; Pred. No. 0.066;
 Matches 102; Conservative 103; Mismatches 169; Indels 123; Gaps 22;

QY 46 CPCQRIQVG---RTINKLFPDLAEEENV-----LDREFLNELDNVRAQ 89
 DB 57 CDALQAEVNEAKALREBIQAKYDVDTQKARIQGELEESKRVLESEQAENEKEQDERE 116
 QY 90 LSKDKERKRS-QVIIDRLRLTEERNATVVS-----KQALGKAEMLCSTLKQMKY 141
 DB 117 QLAAMKRLNSQNIIDVYTKKLEQSEBEVLAAGAIOELTEKLESEKETSTAKTDLA 176
 QY 142 LEQODETKOAEAGRLRSKMTM-----EQIELLQSQLPVEEEMIRDMVGQ- 191
 DB 177 VSKLIDSESTSLKFSDMIEMAKTQLINCEKQDEAVELLKQ-KLEBEVKMMSDVEYQK 235
 QY 192 ---SAYEQLAVYCVSLKKEYENLKEARKAGEVADKLKDLFSSRSKIQTYV---- 240
 DB 236 LLESTSEKQOHAEAIEYKQ---LEEQSS---TENLKAENERN-LKTALESDE 287
 QY 241 -SELDQAKLELKSQKDLQASDKELMSLKKRTLMLOET-----LNPV 283
 DB 288 SSALSSETTKQMAKKELESEKESKSELREGMDRLQVHNAGQDIDKLOKTWELMAKI 347
 QY 284 ASETVDRLVLESPAPVEVNLKLRPSFRDIDLNATFDVTPPARPSSQHGYYEKLCLE 343
 DB 348 AKSTEDE-----KLAREQLAGLEL-NAKEDL-----KVVEE 377


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Db 1311 IEDLKRVEEVEVAKNALAAVOSARHDCDLLRQYEEBEDEAKAELOKMSKANSEVAQM 1370
QY 233 RSKLOT-----VSELDQAKLELSAQKDIOSADKEIYSLKKLTMLQETLNPVASETV 288
Db 1371 RAKYETDAIORTTELEESKKKL--AQR-LQDAESIEAVNSKCSASLEKTK--RIQSEVE 1425
QY 289 DRLV-LESPAVEVNLKRRPSF 310
Db 1426 DLMIDGERANALANLDDKKORNF 1448

RESULT 25
Q9YHD8 PRELIMINARY; PRT: 879 AA.
AC Q9YHD8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
GN MHC-1.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;
RA Hu H., Merrifield P., Atkinson B.G.;
RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
RT Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles.";
RL Dev. Genet. 0:0-0(1999).
DR EMBL: AF097904; AAD13769.1; -
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF01576; Myosin_tail.1.
DR PRINTS: PR00194; TROPOMYOSIN.
FT NON TER 1
SQ SEQUENCE 879 AA; 101710 MW; 1CA56851E968A3D8 CRC64;

Query Match 7.4%; Score 177; DB 13; Length 879;
Best Local Similarity 22.8%; Pred. No. 0.053;
Matches 107; Conservative 82; Mismatches 184; Indels 96; Gaps 19;

QY 45 TPCPCRIQVGRKTTINKLFDLQAEENVL-----DREFLKNELDNVRAQLSQKDKK-- 97
Db 214 TAQRARLQTENGELSRQL-----EKESSLITQLSRGQAFTQCTEFLRQLEETKAKNA 268
QY 98 -----RDSOYIIDLRTLEERNATVVSLOALGKAE-----MCSITLK 137
Db 269 LAHALQSSRHDCDLLRQYEEBEDEAKAELOKMSKANSEVAQMFTKYETDAIORTTELEE 328
QY 138 QMKYLEQOODETQKQAEAGRLRSKMTMEQIELLSQSLPEVEEMTRDMGVGSAVEQL 197
Db 329 AKKTLAQRLE--AEQVEAVNSKCSASLEKTKRLQA---EVEDLWVDVERSSAAL 382
QY 198 -----AVYCVSLKKEYEN-----LKEARAKSEV-----ADKLR----- 226
Db 383 DKKORNFQVLAEMKQKQYEEAQAELESALDKDARMSSTEIFMKNAVEESLDLETLKRN 442
QY 227 -----KDLFSSRSKLTQTYVSELDQAKLELSAQKDIOSADKEIYSLKKLTMLQET 277
Db 443 KNLQOETSLDLEQISEGKTYHELEKAKKLVQEKSDQLQALEBAESLHEESKILRIQ 502
QY 278 LNPVASETVDRLVLESPAVEVNLKRRPSFRDDIDLNATFDVD---TPPARPSSSQ 333
Db 503 LELNQLKSE--VDRKIARKEDETE---QLKRNISQRIIDTMQSTLSEISRNDALRLKKM 558
QY 334 HGTYEKLCLKESHPIQ--DVPKTI--CKGPRKESQSLGQSCAGBDEFLVCAPIFV 389
Db 559 EGDNLELEIQLSHANRQAAEAQKOLRNVOAHLKDNQLQLDD---ALRSQEDLAKQOAVVE 615
```

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QY 390 RNALILQOKOPKRRPS---ESSCKDVVRTGFDGLGRTFKFIQPTDVI 435
Db 616 RRNNLQOAEIETIRSALEOTERSKRYAEOELDASERVQLHNSQNTSLI 664

RESULT 26
Q99MT2 PRELIMINARY; PRT: 976 AA.
AC Q99MT2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE RAB6-INTERACTING PROTEIN 2 ISOFORM A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Monter S., Janoueix-Lerosey I., Jollivet F., Goud B.;
RT "Characterization of a novel interaction partner of the small GTPase
RT Rab6.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF340028; AAK26381.1; -
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR PRINTS: PR00194; TROPOMYOSIN.
SQ SEQUENCE 976 AA; 111931 MW; 48731867C8D8C6F CRC64;

Query Match 7.4%; Score 176.5; DB 11; Length 976;
Best Local Similarity 20.5%; Pred. No. 0.063;
Matches 84; Conservative 77; Mismatches 137; Indels 111; Gaps 14;

QY 8 TICSDFPHSRDYAAIHGHTFHLQCLIOSFETAPRTCPQCRIOVG-----KRTII 59
Db 491 TLNMFQSDSKQ-----HIEVLKESL-TAKEGRAAILQTEVDALRLRLEKETML 538
QY 60 N---KLEFDLAQE-----ENVLDRE-----FLKNELDNVRAQLSQKDKKRSQ 101
Db 539 NKRTKOIQDMAEKEGTQAGEIHDKMLDVKERVNVLQKRIINLEQLKQEKQMSLKL 598
QY 102 VIIDTLRDLTEERNATVVSLOALGKAEMLCSTLKQKMYLEQOODETQKQAEAGRLRS 161
Db 599 ERKSLQADPTNTDPTALTTEBALADKERTIERLK-----EQRDREREKQEEIDITYK 652
QY 162 KMKTMEQIELLSQSLPEVEEMTRDMGVGQS-----AVEQLAVYCV- 202
Db 653 DLKDLREKVSILQGDISEKASILDIDKEHASLSASSGLKKDSRLKLTLELQEKKECKL 712
QY 203 ----SLKKEYENLKEARAKSEVADK--LRKDLFSSRSKLTQTYVSELDQAKLELSAQK 256
Db 713 MESQLKHAHEATLEAR-ASPMSBDRIOLEIREISRYKDESSKAQTEVDRLLETLK 771
QY 257 LQSDAKREIMSL-----KKRLTMLQETLNPVASETVDR 290
Db 772 KNDKDKKIALESLSITSQYVDQKKVYANLKHKEQVEKKKSAQMLEARRRREDSLS 831
QY 291 LVLESPAVEVNLKRRPSFRDDIDLNATFDVDTPPARPSSSQHGYEYK 339
Db 832 LQVE-----ELLMAMEK-----VKQELSEMKAKLSSTQOSLAEK 865
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RESULT 27
Q28714 PRELIMINARY; PRT: 1156 AA.
AC Q28714;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CHROMOSOME SEGREGATION PROTEIN (SMC1).
GN AFI558.
OS Archaeoglobus fulgidus.
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RC STRAIN=LANDRACE; TISSUE=SKETETAL MUSCLE;
 RA Chikuni K., Tanabe R., Muroya S., Nakajima I.;
 RT "differences in molecular structure among the porcine myosin heavy
 chain-2a, -2x, and -2b isoforms.";
 RL Meat Sci. 57:311-317(2001).
 DR EMBL; AB025262; BAA82146.1; -.
 DR HSSP; P13538; 2MYS.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004008; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00193; MIOSINHEAVY.
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 1.
 SQ SEQUENCE 1939 AA; 223172 MW; B702ADB599602ECB CRC64;

Query Match 7.4%; Score 176; DB 6; Length 1939;
 Best Local Similarity 21.5%; Pred. No. 0.14;
 Matches 87; Conservative 81; Mismatches 148; Indels 88; Gaps 16;

QY 31 LQCLIOSEFPAAPSTCQCRCRIQVCKRTIINKLFPDLAQBEEVNDREF----- 78
 DB 1147 LEETSERLEEGAGTSAQIEENKKREAEFOKLRDL--EATLQHEATATLKKHADS 1203
 QY 79 ---LKNELDNVRAQLSQDKREKRDQVYIDPLRDLTEERNATVVSLOALGKAMLCSTL 135
 DB 1204 VAELEGQIDNLQRYKQKLEKSEKMEIDLSNME-----TVSKAKNLEKMCRTL 1256
 QY 136 KQMKYLEQQODEK-----QAQEEAGRL-----RSKMKTMEOI 169
 DB 1257 EDQLSELKTEKEEQRLINDLTAQRARLQTESEYRQLDKPTLVLSQSGKQAFYQOI 1316
 QY 170 ELLIQLSLPEVEEMIRMGVQGSVEQLAVYCVSLKKEYENLKARKASGEVADKLKDL 229
 DB 1317 EELKR---OLEEIKKKSALAHAVQSSRHDCDLRLQYEEQDEQAKELQRAMSKANSEV 1372
 QY 230 FSSRSKLTQ---YSELDQAKLELKSQKDLQSDAKREIMSLKKTMLQETLNLPPVAS 285
 DB 1373 AQWTKKETDAIQRTTELEESKKKL--AQR-LQDAEEHVEAVNAKCSLETKQ--RLQN 1427
 QY 286 ETVDRLV-LESPAVEVNLKLRPSFRDI-----DLNATFDVDTPPARPSSSQ-- 333
 DB 1428 EVEDLMIDIVERSNAACALDKQRNF--DKILAEWKQKEYETTHAELEASQKRSLSLTLEF 1486
 QY 334 ---HGYEKL---CLEKSHPIQ---DVPKKICKGPRKESQL 366
 DB 1487 KVKNAYESLDQLETLKRENKNLQOEISDLTEQIAEGKRRIHEL 1530

RESULT 30
 Q98T06 PRELIMINARY; PRT; 1929 AA.
 AC Q98T06;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 GN MYOHC-A1.
 OS Notothenia coriiceps (black rockcod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Nototheniidae; Nototheniidae; Notothenia.
 OX NCBI_TaxID=8208;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Gauvry L., Emmon S., Etelale C., Goldspink G.;
 RT "Characterisation of red and white muscle myosin heavy chain gene
 coding sequences from Antarctic and tropical fish.";
 RL Comp. Biochem. Physiol. 127:575-588(2000).
 DR EMBL; AJ243767; CAC27776.1; -.
 DR HSSP; P13538; 2MYS.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004008; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00193; MIOSINHEAVY.
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 SQ SEQUENCE 1929 AA; 221167 MW; 20A78CBA19DE851B CRC64;

Query Match 7.4%; Score 175.5; DB 13; Length 1929;
 Best Local Similarity 22.4%; Pred. No. 0.15;
 Matches 73; Conservative 66; Mismatches 122; Indels 65; Gaps 11;

QY 31 LQCLIOSEFPAAPSTCQCRCRIQVCKRTIINKLFPDLAQBEEVNDREF----- 78
 DB 1137 LEETSERLEEGAGTSAQIEESKKREAEFOKLRDL--BESTLQHEATATLKKHADS 1193
 QY 79 ---LKNELDNVRAQLSQDKREKRDQVYIDPLRDLTEERNATVVSLOALGKAMLCSTL 135
 DB 1194 VAELEGQIDNLQRYKQKLEKSEKMEIDLSNME-----NVAKAGNLEKMCRTL 1246
 QY 136 KQMKYLEQQODE-----TQDAEEAGRL-----RSKMKTMEOI 169
 DB 1247 EDQLSELKTNDEVNRQINDTSSQARLITNGEYSQIEKEALVSQLRGKQASTQOI 1306
 QY 170 ELLIQLSLPEVEEMIRMGVQGSVEQLAVYCVSLKKEYENLKARKASGEVADKLKDL 229
 DB 1307 EELKR---HIEEIVKKNALAHGLQSAHRDCDLRLQYEEQDEQAKELQRAMSKANSEV 1362
 QY 230 FSSRSKLTQ---YSELDQAKLELKSQKDLQSDAKREIMSLKKTMLQETLNLPPVAS 285
 DB 1363 AQWTKKETDAIQRTTELEESKKKL--AQR-LQDAEIOIEAVNKAISLETKQ--RLLS 1417
 QY 286 ETVDRLV-LESPAVEVNLKLRPSF 310
 DB 1418 EVEDLMIDIVERANALANLIDKKQRNF 1443

RESULT 31
 Q9QZ84 PRELIMINARY; PRT; 2473 AA.
 AC Q9QZ84;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE LEKI (FRAGMENT).
 GN 6530404A22RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99303627; PubMed=10373470;
 RA Goodwin R.L., Pabon-Pena L.M., Foster G.C., Bader D.;
 RT "The cloning and analysis of LEKI identifies variations in the
 LEK/centromere protein F/mitosin gene family.";
 RL J. Biol. Chem. 274:18597-18604(1999).
 DR EMBL; AF194970; AAF07196.1; -.
 DR MGD; MGI:1915046; 6530404A22RIK.
 FT NON_TER 1 1

SO SEQUENCE 2473 AA; 281903 MW; 504E91A1A150A3E5 CRC64;

Query Match 7.4%; Score 175.5; DB 11; Length 2473;

Best Local Similarity 23.1%; Pred. No. 0.2; Matches 64; Conservative 63; Mismatches 105; Indels 45; Gaps 6;

QY 65 DLAGEEN---VLDREFLNELDNVRAQLSQDKERKDSQVITDRLDTEERNATVVS 120
 DB 1638 ELERSEENQELALIDSENLKAQVETLKAQKDEMTKSLRIFELDLVTATREBNLAKQOE 1697
 QY 121 LQALGKAEMLCSTLKAKKQKLEEO-----ODETKQAGEBGRLSKKKT 165
 DB 1698 KOSRVSSELDKRCSSLRLLKEEQARVOMEDSKSAMLMLQMLKLEEEVAALCNDET 1757
 QY 166 MEOTELLQSQLPVEEEMIRDMGVGQSAVEQLAVYCVSLKREYENLKARKASGEVADKL 225
 DB 1758 LKAGQSLDQGEVYHNH-----KSSIRKLKHAIDDEKKNHILEQLKSKHNDL 1810
 QY 226 R-----KDLF-----SSRSKLQTVSELDQAKLELSAOKDLSADKEIMSL 267
 DB 1811 KDRVENLEQELILSEKNMIFQAEKSKAEIQTLKSEIQHMAQNLQDLQLELSTSEENL 1870
 QY 268 KKKLTMLQETLNLPPVASETVDRVLVLESPAVEYNLK 304
 DB 1871 IKELKEQERVSDELTINPSENL-LKDKOEKQVOMK 1906

RESULT 32

044929 PRELIMINARY; PRT; 1690 AA.

AC 044929;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MICROVIBRIE BINDING PROTEIN D-CLIP-190.
 GN CLIP-190 OR CG5020.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON R;
 RA Lantz V.A., Miller K.G.;
 RL J. Cell Biol. 0:0-0(1998).
 DR EMBL: AF041382; AAB96783.1;
 DR FlyBase: FBgn0020503; CLIP-190.
 DR InterPro: IPR000938; CAP-Gly.
 DR Pfam: PF01302; CAP_GLY; 2.
 SQ SEQUENCE 1690 AA; 189103 MW; BEAF48FD15F17A7C CRC64;

Query Match 7.3%; Score 175; DB 5; Length 1690;

Best Local Similarity 20.9%; Pred. No. 0.14; Matches 84; Conservative 84; Mismatches 157; Indels 76; Gaps 13;

QY 50 RIQVGRITIKLFEDLAAGEENVLDFELKNE--LDNVRASQDKERKDSQVITDRL 107
 DB 724 QIQLEKESIEQL--ALKONLEDFQKKQSEVHLQETIKQONQKDELVESESLEKL 781
 QY 108 RDTLEERNATVVSQALGKAEMLCSTLKQMK-YLEQOODETKQAOEAGRLSKKMTM 166
 DB 782 QQQLEETLGHKEQLAL-----ELKKKEKTIKEKEDELQLOQSKSSESALKVY 834
 QY 167 E-QIETLLQSQLPVEEEMIRDMGVGQSAVEQLAVYCVSLKREY----- 209
 DB 835 QVQLEEQLOQQAASGEGSKTVAKLHDEISQLSQAEETQSGELKSTESNLEAKSKOLEAA 894
 QY 210 --NKEARKASGEVAD--KLRKDLFSSRSKLQTVYSELDAKLELSAOKDLSADKEI 264
 DB 895 NGSLEEKAKSGOLOEQTITKSEVEETQALSSYHTDVESTKQLEAANAALKEKVKKEY 954

QY 265 MSLKKLTMLQETLNLPPVASETVDRVLVLESPAVEYN--TKLRPSPRDDI-----DLN 317
 DB 955 AESRAEASDLDQKY-----KEITDTLHAELQAEKRSSSALHTLSKFSDEIATGHKEIT 1008
 QY 318 ATFDV-----DTPPARSSQHGYYEKLCLKESHSPIDVPKKIC 357
 DB 1009 SKADAWSQEMLQKEKELEQLROQLQDSQDSQTKKACGERKSEFSES---IKNILEEVT 1065
 QY 358 KGPRKESOLSLGQSCAGEPDELVGAFPIFVRRAIIGOKO 398
 DB 1066 KAKTENLELSTGTOTTTKIDLERLE-----ITNAELQHKE 1100

RESULT 33

090PS1 PRELIMINARY; PRT; 529 AA.

AC 090PS1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIAA1081 PROTEIN (FRAGMENT).
 GN KIAA1081.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=9337452; Pubmed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirotsawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB029004; BAA83033.1; -
 DR HSSP: P01100; IFOS.
 DR InterPro: IPR002017; Spectrin.
 FT NON_TER 1
 SQ SEQUENCE 529 AA; 61417 MW; 08D94249ACC63F22 CRC64;

Query Match 7.3%; Score 174.5; DB 4; Length 529;

Best Local Similarity 20.2%; Pred. No. 0.042; Matches 86; Conservative 84; Mismatches 155; Indels 101; Gaps 15;

QY 30 HLCQLQSFETAPSRCTPCRCRIQV-----KRTIIN--KLFDLAQEE----- 70
 DB 11 HIEVLKESL-TAKQRAAILQTEVDALRLLEKEKTMINKKTKQIQDMAEKEGTQAGEIH 69
 QY 71 --ENVLDRE-----FLKNELDNVRAQLSQDKERKDSQVITDRLDTEERNATVVSLOQ 123
 DB 70 DLKMDLVKRRKVVNLQKKTIENLOELRDKQSSLKREYKSLQADTTMTDALTTLEE 129
 QY 124 ALGKAEMLCSTLKQMKYVLEQOODETKQAOEAGRLSKKMTQELLLQSQLPVEEM 183
 DB 130 ALAKEKTIERLK-----EQRODEREKQEBIDNKKDKLQKLEKYSLLQGLSKEKAS 183
 QY 184 IRDMGVGQSAVEQLAVYCVSLKREYENLKARKASGEV 221
 DB 184 LLDLKEHASSIASGLKQDSRLKTLLEIALBQKKEECLKMSQLEKAHEALAEAR-ASPEM 242
 QY 222 ADK--LRKDLFSSRSKLQTVYSELDAKLELSAOKDLSADKEIMSL----- 267
 DB 243 SDRIQHLERBITRYKQDSSKAQAEVDRLEILEVEENEKNDKQKIAELSLSTRQVKQ 302
 QY 268 -----KKKLTMLQETL--NLPPVASETVDRVLVLESPAVEYNLKLRRP 308
 DB 303 NKVYANLKHKEQYKKSQAOMLEARRENLDSSQLODLSLKKDKDRLEEL-----EG 357
 QY 309 SFRDDIDLNATFDV--DTPPARSSQHGYYEKLCLKESHSPIDVPKKICGKPR--- 361

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Db 358 ALRESVQITAREVYLAQESARFNAEKOVBELIMAMEKVQOELESMKAKLSTQOSLAE 417
QY 362 KESOLS 367
Db 418 KETHLT 423

RESULT 34
P87344
ID P87344 PRELIMINARY; PRT: 1119 AA.
AC P87344;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Theragra chalcogramma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
OC Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST MUSCLE;
RA Togashi M., Hirayama Y., Kakinuma M., Watabe S., Ojima T., Nishita K.;
RT "cDNA cloning of Alaska pollock fast skeletal muscle myosin heavy
RT chain.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000214; BAA19070.1; -.
DR HSP; P13538; 2MYS.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 1119 AA; 128626 MW; B8C5FECAE6F5B954 CRC64;

Query Match 7.3%; Score 174.5; DB 13; Length 1119;
Best Local Similarity 23.9%; Pred. No. 0.094;
Matches 79; Conservative 63; Mismatches 115; Indels 73; Gaps 13;

QY 31 LQCLISQFETAPSRPCRCIOVGKRTITNKLFPDLAGEENVLDREP----- 78
Db 327 LEETSERLEEGGATSAQIEMKKREAFQKLRDL---ESTLQHEHTAALKKQADS 383
QY 79 ---LKNELDNVRAQLSOKDEKRDQVLIIDLRDLEERNATVVSLOALGKAEMLCSTL 135
Db 384 VAEIGEOIDNLQRYKQKLEKSEKMEIDLSNME-----AVSKAKGNLEKICAL 436
QY 136 KKQKLYLEQODETKQAOEAGRLSKMKT-----MEQIELL-----OSQLEPY 180
Db 437 EDQLEIKAKDENARQVNDISAQRARLTNGEGRQLEKALVSQLTRGKQAYTVQV 496
QY 181 EEMTRDMGVGSAVEOLA-----VYCVSLKREYENLEKAR-----KASGEVADKL 225
Db 497 EELKRONEEVAKNALAHGVOSARHCDLREQFEQEKAKELQKMSANGEVA--- 553
QY 226 RKDLFFSRSLQOT---VYSELDAQLELKSQAKDQASADKEIMSLKRLTMLQETLNP 281
Db 554 -----QWRSKYETDAIQRTLEESKKKL--AQR--LQEAEPQIEAVNSKASLEKTKQ-- 603
QY 282 PVASTVDRLV--LESPAVYEVNKLRRPSF 310
Db 604 RLQGEVEDLWVDERANGLANLDKKRNF 633

RESULT 35
Q9YHD4 PRELIMINARY; PRT: 671 AA.
AC Q9YHD4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
GN MHC-5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;
RA Hu H., Merrifield P., Atkinson B.G.;
RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
RT Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles.";
RL Dev. Genet. 0:0-0(1999).
DR EMBL; AF097908; AAD13773.1; -.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 671 AA; 78062 MW; 1904A262790CA26F CRC64;

Query Match 7.3%; Score 174; DB 13; Length 671;
Best Local Similarity 21.9%; Pred. No. 0.058;
Matches 106; Conservative 92; Mismatches 167; Indels 118; Gaps 20;

QY 68 QEEENVLD-----REFLKNELDNVRAQLSOKDEK-----RDSQVLIIDLRDLEERN 115
Db 30 EKSLSVQSQRQAPATQOEELKRLQLEETFKNALAHVQSARHCDLRLRQYEEDQ 89
QY 116 ATVVSLOALGKAMLC-----TLKQKMYLEQODETKQAOEAGRLR 160
Db 90 EAKAELQRLSKANSEVSWRTKYETDAIQRTLEELKAKKLAQRLQE---AEQILEAVN 146
QY 161 SKMKTMEQIELLQSLPEVEEMIRDMGVGSAVEOLAAYCVSLKKEYNL----- 211
Db 147 SKCASLETKORLQA---EVEDLWVDRSNSA-----CTALDKKQKNFYKVLSEMKQ 196
QY 212 -----KEARKASGEVADKLRLKDLFFSRSLQTV----- 239
Db 197 KYEAQAELEAKQESKRLSTFEV-KMKNNYEALDQLETLKRNKNLQOESLDTBOVA 255
QY 240 -----YSELDAQLELKSQAKDQASDEIN-SLK-KKLTMLQETLNPVASTVDRLV 292
Db 256 ESGKSIHEIEKAKQOVEQEKSELQSALEAAGSLHEBEAKILRVQLEINQKSE--VDRKV 314
QY 293 LESPAPVEVNLKLRRPSRDDIDLNATFDVD---TPPARSSSOHGYYEKLCEKSHSP 348
Db 315 AEKDEEIE--QLKNSQRALESQTSLSQSEVSRNDALRLKMKMEGLNMEQLSHAN 371
QY 349 IQ--DVPEKTI--CGPRKESQSLGSGSCAGEPDELVGAFIPFVNAIIGOKPRPRS 404
Db 372 RQAABEQKLLNNGVQGFDAQLHLD--AIRGNLDKEQLAIYERRNNMLQATIEEMRS 428
QY 405 ---ESSCKDQVVRIGFDLGRTFTIOPDTVMIRPLPVAKRTYVKQVRKYTVPSLFOA 461
Db 429 ALQETERRKVAHEHLLDVTERRVOLLHTQNTSLI-----NFKKLEADV---SOFOS 477
QY 462 KLD 464
Db 478 EVD 480

RESULT 36
Q98TQ5 PRELIMINARY; PRT: 975 AA.
AC Q98TQ5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
```

DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN MYOHC-A3 GENE.
 OS Notothenia coriiceps (black rockcod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Notoleosteoi;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 CC Notothenioidae; Nototheniidae; Notothenia.
 OX NCBI_TaxID=8208;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gavray L., Emmon S., Etteleat C., Goldslink G.;
 RT "Characterisation of red and white muscle myosin heavy chain gene
 RT coding sequences from Antarctic and tropical fish.";
 RL Comp. Biochem. Physiol. 127:575-588(2000).
 DR EMBL; AJ243768; CAC27777.1; .
 DR HSSP; P03437; IHTM.
 DR InterPro; IPR002928; Myosin_tail.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR NON_TER 1
 FT SEQUENCE 975 AA; 112313 MW; 2F7AD46A3419537F CRC64;

Query Match 7.3%; Score 173.5; DB 13; Length 975;
 Best Local Similarity 22.1%; Pred. No. 0.092;
 Matches 72; Conservative 67; Mismatches 122; Indels 65; Gaps 11;

QY 31 LQCLQSETAPSRCTPCRCIOVGKRTTIINKLFPDLAEEENVLDREF----- 78
 Db 183 LEEISERLEEAGATSAQIEENKKEAEFORLRLDL---EESTLOHEHTASALRKQADS 239
 QY 79 ---LKNELDNVRAQLSOKDKERDSQVITLRLDTLEERNATVYSLQALKAEMLCSTL 135
 Db 240 VAELEQEDINLQKVKQKLEKESEKMEIDLSNME-----NVAKAKNLEKMCRTL 292
 QY 136 KKQMYLEEQODE-----TKQAEAGRL---RSKMTMEOI 169
 Db 293 EDQFSELTKTKDENVRQINDTSSQKARLITENGESRQVEKEALVSLTGKQASTQOI 352
 QY 170 ELLIQLSOLPEVEEMIRDMGVQSAVEQLAVYCVSLKKEYENLKEKRAKSGEADKLRDL 229
 Db 353 DELKR---QIEEVKAKNALAHGLQSAHRHDCDLRLEQFEEOEKAKELQKMSANSEV 408
 QY 230 FSSRSKLTQ---VYSELQAKLELSAQKDLQSADEKIMSUKKLTLMQETLNLPPVYS 285
 Db 409 AQMSKSYETDNLQRTLEELSESKKL--AQR-LQEAHQIEAVNSKCSLEKTKQ--RLQS 463
 QY 286 ETVDRLV-LESPAPVEVNLKLRPSF 310
 Db 464 EVEDLMDIVERANALANLDRKQRF 489

RESULT 37
 096063 PRELIMINARY; PRT; 1743 AA.
 AC 096063;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN DJMHC-B.
 OS Dugesia japonica (Planarian).
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Serjata; Tricladida;
 OC Paludicola; Dugesidae; Dugesia.
 OX NCBI_TaxID=6161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kobatashi C., Agata K., Orli H.;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 DE SEQUENCE FROM N.A.
 RA Kobayashi C., Kobayashi S., Orli H., Agata K., Watanabe K.;

RT "Identification of two distinct muscles in the planarian, Dugesia
 RT japonica, by the expression of myosin heavy chain genes.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GTR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL; AB015485; BAA34955.1; .
 DR HSSP; P08799; IMND.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR001637; Glna_adenyltn.
 DR InterPro; IPR000524; HTH_GntR.
 DR InterPro; IPR000048; IQ.
 DR InterPro; IPR001609; myosin_head.
 DR InterPro; IPR002928; myosin_tail.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00035; HTHGTR.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR Prodom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00182; Glna_ADENYLATION; UNKNOWN_1.
 DR PROSITE; PS0096; IQ; 1.
 KW DNA-binding; Transcription regulation.
 FT NON_TER 1
 FT SEQUENCE 1743 AA; 200417 MW; 0D4A821FA6CF7C2 CRC64;

Query Match 7.3%; Score 173.5; DB 5; Length 1743;
 Best Local Similarity 22.6%; Pred. No. 0.17;
 Matches 94; Conservative 75; Mismatches 160; Indels 87; Gaps 16;

QY 51 IQVGKRTTIINKLFPDLAEEENVLDREFLKNELDNVRAQLSOKDKER-----RDSQVI 103
 Db 839 VEKAKR-----KVEGELKQNMELNDLEKSELSE---QLKRRKMEIANGANSKLTEDENNL 891
 QY 104 IDTLRLDTLEERNATVYSLQ-----QALGKAEMLCSTLKKQMYLYEQODE---TQAO 153
 Db 892 VATLQKRIKELQARIQIELEDLEAERQARAERAKHQLEAEIEVEERLEEQAGATQAO 951
 QY 154 EEAQRLS---KMK-----TMEQIELLOS-----QLEPEV---EMIRD 186
 Db 952 TDLAKKRAEELMKLRQLEERNMHEQAINGTRKKODTANEFADQDQDQKSKITERE 1011
 QY 187 MGVQSAVEQLAVYCVSLKKEYENLKEKRAKSGEADKLRDLFSSRSKLTQYVSELQQA 246
 Db 1012 KNEIRGDIEDLSGOLESINKAKIMLEKSNKGLFATISLQNKLDLTKQLSDAGNSNNRN 1071
 QY 247 KLELSAQKDLQSADEKIMLSUKKLTLMQETLNLPPVASEYVDVLYLESPAPVEVNLKLR 306
 Db 1072 QHENSELKSLEDAESQINQSLKAKQQLQAL-----EEAKQNLDESESRKSKLTNGLDLR 1125
 QY 307 RPSFRDDILNATPDVDTPPARPSSOHGYEKLKLSKSPIDQVPKIKCKGPKRESQL 366
 Db 1126 -----NALSDLA--MRES-----LEEDEGKSDVGRQLVKNQNELOQL 1162
 QY 367 SLGQSCAGEPEDELVGAPLIVR--NALIGQKPKRPRSESSCSK--DYVRTGFDG 419
 Db 1163 KNSQGTGTVGRSEEM-----EEFKRKMARIQLEEESESNKSKSQLEKVSRLQG 1214

RESULT 38
 09AMC4
 ID 09AMC4 PRELIMINARY; PRT; 437 AA.
 AC 09AMC4;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE M18 PROTEIN.
 GN EMM18.2.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 RT Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eschaki M., Manaf A., Yusoff K., Jamal F.;
 RT "Sequence Analysis of the 5' Region of the emm Gene of Group A
 Streptococci Isolates from Malaysia."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF326566; AKK11617.1; -
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR003345; M_repeat.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF02370; M; 9
 DR PRINTS: PR00015; GPOSANCHOR.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 KW Transmembrane.
 SQ SEQUENCE 437 AA; 48849 MW; F1D1F586567EDDB CRC64;

Query Match 7.3%; Score 173; DB 2; Length 437;
 Best Local Similarity 22.9%; Pred. No. 0.041;
 Matches 77; Conservative 67; Mismatches 140; Indels 52; Gaps 11;

OY 66 LAQEEENVLDREFL---KNE-----LDNVAQLSQKKEKRDSDVITDRLD 109
 DB 105 LATOKEN-LEKEYEAKHKKETLINNDLTCLKINETROELANKQDSKENE---KTLNE 160
 OY 110 TLEERNATVVSLOALGKAMLCSTLKKOMKYLEQOODETKQAOE-----EAGRLRSKM 163
 DB 161 LLEKTVYKDKIAREQ---KSKQDFGALNQELAKKEQKISDASRKGRLRDLASREAKKQ 217
 OY 164 KTMEOIELLQSQLPVEE--MIRDAGVGSAYBQLAVYCVSLAKEVENLKEAKAGCEV 221
 DB 218 LEAEHQLEBQNKISESRKGRGLRDLASREAKQYVEKDLANLTAELDKYKEEQISDAS 277
 OY 222 ADKLKRDLFSSRSKLTQVYSELDOAKLELKSQAOKLSADKEIKSLKLTMLQETLNP 281
 DB 278 RQGISRLLEASREYKKEVADLAENSKLSPLKNLTKSLKKNYKOK-KLLSSRRLE 336
 OY 282 PVASETVRLVLESPAVEYNLKLRRPSFRDDIDLNTFVDPVPPARPSSOHGYEKLK 341
 DB 337 AEAKALKEQLAKQA---EELAKLR-----AGKASDSQFPAKPGN-----KVV 376
 OY 342 LEKSHSPIQDVPPKTKCGPKKESQLSGGSCAGEP 377
 DB 377 PGKQAPQAGCTKPNONKAPMKETKRQLPSTGGAANP 412

RESULT 39
 099M11 PRELIMINARY; PRT; 1120 AA.
 AC 099M11;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RAB6-INTERACTING PROTEIN 2 ISOFORM B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Monter S., Janoueix-Lerosey I., Jollivet F., Goud B.;
 RT "Characterization of a novel interaction partner of the small GTPase
 Rab6."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF340029; AAK26382.1; -
 DR InterPro: IPR002017; Spectrin.
 SQ SEQUENCE 1120 AA; 128330 MW; A542B526FAEDF9C7 CRC64;

Query Match 7.3%; Score 173; DB 11; Length 1120;
 Best Local Similarity 19.6%; Pred. No. 0.11;
 Matches 87; Conservative 88; Mismatches 165; Indels 104; Gaps 15;

OY 8 TICSDFPHSRDVAIHCHGTHFLQCLIOSFETAPSPQCRIOVG-----KRTII 59
 DB 491 TLTNQFSDSKQ-----HIEVLKESL-TAKEDRAAILQTEVDALRLREKEETML 538
 OY 60 N---KLFDLAQRE-----ENVLDRE-----FLKHELDNVAQLSQKKEKRDQ 101
 DB 539 NKRTKQIQDMAEKGQAGEIHDLKMLDVKEKRVVNLQKRIENLQEQLEKKEKQMSLK 598
 OY 102 VIIDTLRDTLEERNATVVSLOALGKAMLCSTLKKOMKYLEQOODETKQAOEAGRLRS 161
 DB 599 ERKKSILQADQTNDFALTLTEALADKERIETRLK-----EQRDRERKQGEIETYKK 652
 OY 162 KMTMEQIELLQSQLPVEEEMIRDMGVGS-----AVEQLAVCV- 202
 DB 653 DLKDLREKVSLLQGDSEKEASLIDIKENHASSLASSGLKKDSRLKTLLELQKKEECLK 712
 OY 203 ---SLKKEYNLKEARKAGEVADK---LRKDLFSSRSKLTQVYSELDOAKKLEKSAOKD 256
 DB 713 MESQLKHAHATLEAR-ASPEMSDRIQLEIREISRYKDESSKAQTEVDRLLEIKVEENE 771
 OY 257 LQSADEKIMSL-----KKKLTMLQETLNPVASETVDR 290
 DB 772 KNDKDKKIALLESITSNQVADQKKYANLKHKEQVEKKAQMLEKRRRDELSDSQO 831
 OY 291 LVLESPAVEYNLKLRRPSFRDDIDLNTFVDPV---DTPARPSSOHGYEKLKESHS 347
 DB 832 L-QDSLKKKDDRIEELAEALRESQVLAERENVLAQESARTNAKQVELELLAMEKVKQ 890
 OY 348 PIQDVPPKTKCGR---KESQLS 367
 DB 891 ELESMAKLSSTQOQSLAEKETHLT 914

RESULT 40
 099HD7 PRELIMINARY; PRT; 708 AA.
 AC 099HD7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN MYC-2.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;
 RA Hu H., Merrifield P., Atkinson B.G.;
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
 Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles."
 RL Dev. Genet. 0:0-0(1999).
 DR EMBL: AF097905; AAD13770.1; -
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00194; TROPOMYOSIN.
 FT NON_TER 1
 SQ SEQUENCE 708 AA; 81824 MW; BE2D017000179C4C CRC64;

Query Match 7.2%; Score 172.5; DB 13; Length 708;
 Best Local Similarity 22.7%; Pred. No. 0.074;
 Matches 93; Conservative 83; Mismatches 142; Indels 91; Gaps 19;

OY 45 TPCQCRIOVGKRTIINKLFDLQAEENVLD---REFLKNELDNVAQLSQKKEK-- 97
 DB 47 TTPARALQTENGELSRQL-----EKEKSLISQLSRGKIGFTQGVVEELKRLQLEESKAKNA 101

